



1

SEQUENCE LISTING

RECEIVED

MAR 26 2001

TECH CENTER 1600/2900

<110> MORI, SATOSHI
NAKANISHI, HIROMI
OKI, HIROYUKI
YAMAGUCHI, HIROTAKA

<120> METHOD FOR TRANSFORMING PLANT, THE RESULTANT PLANT AND
GENE THEREOF

<130> 55022 (71526)

<140> 09/646,825
<141> 2000-09-22

<150> JP/10-96637
<151> 1998-03-24

<160> 38

<170> PatentIn Ver. 2.1

A^y
<210> 1
<211> 2092
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
saccharomyces cerevisiae

<220>
<221> CDS
<222> (20) .. (2077)

<400> 1
gaatttctcta gactccacc atg gtt aga acc aga gtc ctt ttc tgc ctc ttc 52
Met Val Arg Thr Arg Val Leu Phe Cys Leu Phe
1 5 10

atc tct ttc gct aca gtc caa tcg agc gct aca ctc atc tcc act 100
Ile Ser Phe Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr
15 20 25

tca tgc att tct cag gct gca ctg tac cag ttc gga tgc tca agc aag 148
Ser Cys Ile Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys
30 35 40

tca aag tct tgc tac tgc aag aac atc aat tgg ctc gga agc gtc act 196
Ser Lys Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr
45 50 55

gca tgc gct tat gag aac tcc aaa tct aac aag act ctg gac tcc gct 244
Ala Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala
60 65 70 75

ttg atg aaa ctt gcc agc caa tgc tca agt atc aag gtt tac aca ctg 292
 Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu
 80 85 90

gag gac atg aag aac atc tac ctt aat gca agt aac tac ctt cgc gct 340
 Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala
 95 100 105

cct gag aaa tcc gat aag aag aca gtt gtt tca caa ccg ttg atg gca 388
 Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala
 110 115 120

aat gag acg gcc tat cac tac tac tat gag gaa aac tat ggg atc cac 436
 Asn Glu Thr Ala Tyr His Tyr Tyr Glu Glu Asn Tyr Gly Ile His
 125 130 135

ttg aat ttg atg cga tct caa tgg tgc gca tgg ggc ctc gtc ttc ttc 484
 Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe
 140 145 150 155

^{A1}
 tgg gtc gca gtc ctt acc gcc gca act atc ttg aac att ctc aaa cgc 532
 Trp Val Ala Val Leu Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg
 160 165 170

gta ttc ggc aag aac att atg gca aat tct gtt aag aag tct ctt atc 580
 Val Phe Gly Lys Asn Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile
 175 180 185

tac cca agc gtt tac aaa gac tac aac gag aga act ttc tat ctt tgg 628
 Tyr Pro Ser Val Tyr Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp
 190 195 200

aaa cgt ttg cca ttc aac ttt aca act cga ggc aaa gga ctc gta gtt 676
 Lys Arg Leu Pro Phe Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val
 205 210 215

ctt atc ttt gtc att ctg act att ctc tca ctc tct ttc gga cat aac 724
 Leu Ile Phe Val Ile Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn
 220 225 230 235

atc aag ttg cca cat cct tac gat aga cct aga tgg aga aga tca atg 772
 Ile Lys Leu Pro His Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met
 240 245 250

gca ttc gtc tca cgc cgt gct gac ttg atg gca atc gct ctt ttc ccc 820
 Ala Phe Val Ser Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro
 255 260 265

gtg gtg tac ctt ttc ggt atc cgg aac aac ccc ttc atc cca atc acc 868
 Val Val Tyr Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr
 270 275 280

gga ttg agc ttt agt act ttc aac ttt tac cac aaa tgg tca gca tac 916
 Gly Leu Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr
 285 290 295

gtc tgc ttc atg tta gcc gtc gtc cat tca atc gtt atg acc gct tca Val Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser 300 305 310 315	964
gga gtt aaa cga gga gta ttc cag tct ctt gta agg aaa ttc tac ttc Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe 320 325 330	1012
aga tgg gga ata gta gcc aca att ctt atg tcc atc atc att ttc cag Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln 335 340 345	1060
tcc gag aag gtc ttc agg aac cga ggt tat gaa atc ttc tta ctt att Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile 350 355 360	1108
cac aaa gcc atg aac atc atg ttt atc ata gct atg tat tac cat tgc His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys 365 370 375	1156
cac aca cta gga tgg atg ggc tgg atc tgg tcc atg gct ggc atc ctc His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu 380 385 390 395	1204
tgc ttc gac agg ttc tgc cga att gta cgt atc atc atg aac gga ggt Cys Phe Asp Arg Phe Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly 400 405 410	1252
ctt aag acc gcc act ttg tcg acc aca gat gat tct aac gtt atc aag Leu Lys Thr Ala Thr Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys 415 420 425	1300
atc tct gtc aag aag cct aag ttc ttc aag tat caa gtg gga gca ttt Ile Ser Val Lys Lys Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe 430 435 440	1348
gcc tat atg tac ttt ctt tca cca aaa tca gcc tgg ttc tac agt ttt Ala Tyr Met Tyr Phe Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe 445 450 455	1396
caa tct cat ccc ttc aca gtc cta tca gaa agg cac aga gat cct aac Gln Ser His Pro Phe Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn 460 465 470 475	1444
aac cca gat caa cta act atg tac gtc aaa gct aac aag ggc att acg Asn Pro Asp Gln Leu Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr 480 485 490	1492
aga gta ctt ctt agc aaa gtt cta agc gct cca aac cat acc gtt gat Arg Val Leu Leu Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp 495 500 505	1540
tgc aag att ttc tta gag gga cca tat ggc gta act gtc cct cac att Cys Lys Ile Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile 510 515 520	1588

gcc aaa ctt aag aga aat cta gta gga gta gct gcg ggc ctc ggc gtg Ala Lys Leu Lys Arg Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val 525	530	535	1636	
gca gcc atc tac ccc cat ttc gta gaa tgc ctt aga ttg cct agc act Ala Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr 540	545	550	555	1684
gat caa ctg cag cac aag ttc tac tgg atc gtc aac gac ctt agt cac Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His 560	565	570	1732	
ctt aag tgg ttc gaa aac gag cta caa tgg ctt aag gag aaa tct tgt Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys 575	580	585	1780	
gaa gtc tct gtc atc tac act ggg tca tca gtg.gag gat aca aac tca Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser 590	595	600	1828	
gat gag tcc act aag ggt ttc gat gac aag gaa gaa tct gaa atc acc Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr 605	610	615	1876	
gta gaa tgc ctt aac aag agg cca gac ctc aaa gag cta gtg aga tca Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser 620	625	630	635	1924
gag atc aaa ttg tca gaa ctc gag aac aac aac atc act ttc tac tca Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn Ile Thr Phe Tyr Ser 640	645	650	1972	
tgc gga cca gcg act ttc aat gac gac ttt agg aat gca gtt gta caa Cys Gly Pro Ala Thr Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln 655	660	665	2020	
ggt atc gat tct agt ctg aag ata gat gtc gaa cta gag gag gag agt Gly Ile Asp Ser Ser Leu Lys Ile Asp Val Glu Leu Glu Glu Ser 670	675	680	2068	
ttt act tgg taagagctca agctt Phe Thr Trp 685			2092	

<210> 2
<211> 686
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
saccharomyces cerevisiae

<400> 2
Met Val Arg Thr Arg Val Leu Phe Cys Leu Phe Ile Ser Phe Phe Ala
1 5 10 15

Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr Ser Cys Ile Ser Gln
 20 25 30

Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys Ser Cys Tyr
 35 40 45

Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala Cys Ala Tyr Glu
 50 55 60

Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala Leu Met Lys Leu Ala
 65 70 75 80

Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu Glu Asp Met Lys Asn
 85 90 95

Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala Pro Glu Lys Ser Asp
 100 105 110

Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala Asn Glu Thr Ala Tyr
 115 120 125

His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His Leu Asn Leu Met Arg
 130 135 140

Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe Trp Val Ala Val Leu
 145 150 155 160

Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg Val Phe Gly Lys Asn
 165 170 175

Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr
 180 185 190

Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe
 195 200 205

Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile
 210 215 220

Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
 225 230 235 240

Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser Arg
 245 250 255

Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr Leu Phe
 260 265 270

Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu Ser Phe Ser
 275 280 285

Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val Cys Phe Met Leu
 290 295 300

Ala Val Val His Ser Ile Val Met Thr Ala Ser Gly Val Lys Arg Gly
 305 310 315 320

Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe Arg Trp Gly Ile Val
 325 330 335
 Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln Ser Glu Lys Val Phe
 340 345 350
 Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile His Lys Ala Met Asn
 355 360 365
 Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys His Thr Leu Gly Trp
 370 375 380
 Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu Cys Phe Asp Arg Phe
 385 390 395 400
 Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr
 405 410 415
 Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys
 420 425 430
 Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe
 435 440 445
 Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe Gln Ser His Pro Phe
 450 455 460
 Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn Asn Pro Asp Gln Leu
 465 470 475 480
 Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr Arg Val Leu Leu Ser
 485 490 495
 Lys Val Leu Ser Ala Pro Asn His Thr Val Asp Cys Lys Ile Phe Leu
 500 505 510
 Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile Ala Lys Leu Lys Arg
 515 520 525
 Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val Ala Ala Ile Tyr Pro
 530 535 540
 His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr Asp Gln Leu Gln His
 545 550 555 560
 Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His Leu Lys Trp Phe Glu
 565 570 575
 Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys Glu Val Ser Val Ile
 580 585 590
 Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser Asp Glu Ser Thr Lys
 595 600 605
 Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr Val Glu Cys Leu Asn
 610 615 620

Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser Glu Ile Lys Leu Ser
 625 630 635 640

Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser Cys Gly Pro Ala Thr
 645 650 655

Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln Gly Ile Asp Ser Ser
 660 665 670

Leu Lys Ile Asp Val Glu Leu Glu Glu Ser Phe Thr Trp
 675 680 685

<210> 3

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

gactcgagtc gacatcg

17

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 4

acacttatta gcacttcatg tatt

24

<210> 5

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

gaattctcta gactccacca tggtagaac cagagtcctt ttctgcctct tcatctcttt 60
 cttcgctaca gtccaaatcga gcg 83

<210> 6

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 6
gtccaatgca gcgctacact catctccact tcatgcattt ctcaggctgc actgtaccag 60
ttcggatgct caagcaagtc aaa 83

<210> 7
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
caagcaagtc aaagtcttgc tactgcaaga acatcaattt gctcggaaagc gtcactgcat 60
gcgccttatga gaactccaaa tct 83

<210> 8
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
tccagtgtgt aaaccttgat acttgagcat tggctggcaa gtttcatcaa agcggagtcc 60
agagtcttgt tagatttggaa gtt 83

<210> 9
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
tgtcttctta tcggatttct caggagcgcg aaggtagtta cttgcattaa ggttagatgtt 60
cttcatgtcc tccagtgtgt aaa 83

<210> 10
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
ggatcccata gtttcctca tagtagtagt gataggccgt ctcatttgcc atcaacggtt 60
gtgaaacaac tgtcttctta tcg 83

<210> 11

<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ggatccacctt gaatttgatg cgatctcaat ggtgcgcatalog gggcctcg 60
tcgcagtcct taccggcgca 80

<210> 12
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ccttaccggcc gcaactatct tgaacattct caaacgcgta ttccggcaaga acattatggc 60
aaattctgtt aagaagtctc 80

<210> 13
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
gttaagaagt ctcttatcta cccaaaggctt tacaaagact acaacgagag aactttctat 60
ctttggaaac gtttgcatt 80

<210> 14
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
agagtggagag aatagtcaga atgacaaaga taagaactac gagtccttg cctcgagttg 60
taaagttgaa tggcaaacgt 80

<210> 15
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
aatgccattg atcttctcca tctaggtcta tcgtaaggat gtggcaactt gatgttatgt 60
ccgaaagaga gtgagagaat 80

<210> 16
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
tccgataacc gaaaaggtac accacgggga aaagagcgat tgccatcaag tcagcacggc 60
gtgagacgaa tgccattgat 80

<210> 17
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
tccggaacaa ccccttcate ccaatcacccg gattgagctt tagtactttc aacttttacc 60
acaatggtc agcatacgtc tgc 83

<210> 18
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
gcatacgtct gcttcatgtt agccgtcgct cattcaatcg ttatgaccgc ttcaggagtt 60
aaccgaggag tattccagtc tct 83

<210> 19
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
tattccagtc tcttgtaagg aaattctact tcagatgggg aatagttagcc acaattctta 60
tgtccatcat cattttccag tcc 83

<210> 20
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ataaacatga tgttcatggc tttgtgaata agtaagaaga tttcataacc tcggttccctg 60
aagaccttct cggactggaa aat 83

<210> 21
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
gaggatgcc a ggcattggacc agatccagcc catccatcct agtgtgtggc aatggtaata 60
catagctatg ataaacatga tgt 83

<210> 22
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
gtcgacaaag tggccgtctt aagacctccg ttcatgtatg tacgtacaat tcggcagaac 60
ctgtcgaagc agaggatgcc agc 83

<210> 23
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
gtcgaccaca gatgattcta acgttatcaa gatctctgtc aagaagccta agttcttcaa 60
gtatcaagtggagcatttg cc 82

<210> 24
<211> 82
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24
ggagcatttg cctatatgt a ctttcttca cccaaaatcag cctgggtct a cagtttcaa 60
tctcatcct tcacagtct at 82

<210> 25
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ttcacagttcc tatcagaaag gcacagagat cctaacaacc cagatcaact aactatgtac 60
gtcaaagcta acaaggcat ta 82

<210> 26
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
cctctaagaa aatcttgcaa tcaacggtat ggtttggagc gcttagaact ttgctaagaa 60
gtactcttgt aatgcccttg tt 82

<210> 27
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
ggcccgccagc tactctact agatttctct taagtttggc aatgtgaggg acagttacgc 60
catatggtcc ctctaagaaa at 82

<210> 28
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
ctgcagttga tcagtgttag gcaatctaag gcattctacg aaatgggggt agatggctgc 60
cacgcccagg cccgcagcta ct 82

<210> 29
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
ctgcagcaca agttctactg gatcgtaac gaccttagtc accttaagtg gttcgaaaac 60
gagctacaat ggcttaa 77

<210> 30
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
acaatggctt aaggagaaat cttgtgaagt ctctgtcatc tacactgggt catcagtgg 60
ggatacaaac tcagatg 77

<210> 31
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
caaactcaga tgagtcact aagggttcg atgacaagga agaatctgaa atcaccgtag 60
aatgcctaa caagagg 77

<210> 32
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
tgatgttgtt tgttctcgag ttctgacaat ttgatctctg atctcaactag ctctttgagg 60
tctggccctct tgtaag 77

<210> 33
<211> 77
<212> DNA
<213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
cgatacctg tacaactgca ttccctaaagt cgtcattgaa agtcgctgg 60
agaaagtgtat gtttgtg 77

<210> 34
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
aagcttgagc tcttaccaag taaaactctc ctcctcttagt tcgacatcta tcttcagact 60
agaatcgata ccttgta 77

<210> 35
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
gactcgagtc gacatcgatt tttttttttt ttttt 35

<210> 36
<211> 2059
<212> DNA
<213> Saccharomyces cerevisiae

<400> 36
atggtttagaa cccgtgtatt attctgctta tttatatctt tttttgctac gttcaatcg 60
agtgcgtacac ttatttagcac ttcatgtatt tcccaagctg cgctatacca atttggatgt 120
tctagtaaat ctAAAAGTTG ctactgtaaa aacatcaatt ggctgggttc agtgcacagca 180
tgtgcctatg agaattccaa atctaacaaa acactagaca ggcgccttaat gaagtttagca 240
tcccataatgtt caagcatcaa agtttatact ttagaggaca tgaagaatat ttatTTAAAT 300
gcgtcaaatt atttggagagc acctgagaaa agtgcataaaa aaaccgtgg tagtcaacccg 360
ctcatggcga acgagacagc gtatcattat tattatgagg aaaatttatgg tatccatctt 420
aacctaattgc gctctcaatg gtgcgttgg ggtctcgct tcttctgggt gggtgtgctt 480
actgcagcca ctatctgaa cattctgaaa agggtgtttg gtaagaacat catggcaaac 540
tccgtcaaaa aatcaattat ttatcctct gttacaag attataatga acgaacttt 600
tatttatgaa agcgtctacc atttaattt acaactcgag gcaagggtct cgctgtat 660
atTTTGTAA TTTTGACTAT attatctctc agttttggtc ataataattaa acttccacac 720
ccatatgata ggcccaagatg gagaagaagt atggccttt tgagtcgtag agcagactg 780
atggccattg cactttccc agtagtctat ctatTCGGAA taagaataaa tcccttcattc 840
cctataacag ggcttcctt ttctacattt aatttctatc ataaatggtc tgcctacgtt 900
tgTTTGTATG TGGCGTTGT acactcaatt gtcatgaccg cctcgggagt gaaaagaggt 960
gtgtttcaaa gtctggtag gaaattttac ttttaggtggg gtatagtggc aacgatatta 1020
atgtctatta ttatTTCCA aagtgaaaaa gtatTTGAA atagagggtt tgagatattc 1080
cttcttattc ataaagcgat gaatattatg ttcattattt ccattgtacta ccattgtcac 1140

```

```
<210> 37
<211> 180
<212> DNA
<213> Saccharomyces cerevisiae
```

<220>
<221> CDS
<222> (1)..(180)

<400> 37
tcc gtc aaa aaa tca ctt att tat cct tct gtt tac aaa gat tat aat 48
Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr Lys Asp Tyr Asn
1 5 10 15

```

gaa cga act ttt tat tta tgg aag cgt cta cca ttt aat ttt aca act   96
Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
          20           25           30

```

cga ggc aag ggt ctc gtc gta tta att ttt gtt att ttg act ata tta 144
Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
35 40 45

tct ctc agt ttt ggt cat aat att aaa ctt cca cac 180
Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
50 55 60

<210> 38
<211> 60
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 38
Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr Lys Asp Tyr Asn
1 5 10 15

Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
 20 25 30

Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
35 40 45

A¹

Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
50 55 60
